

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/806,110

DATE: 04/04/2001  
TIME: 11:17:59

Input Set : A:\1770-214PCT.TXT  
Output Set: N:\CRF3\04042001\I806110.raw

ENTERED

4 <110> APPLICANT: MCGILL UNIVERSITY  
5 KARAPLIS, Andrew C.  
6 GOLTZMAN, David  
7 LIPMAN, Mark L.  
8 HENDERSON, Janet E.  
14 <120> TITLE OF INVENTION: USE OF PEX IN THE TREATMENT OF METABOLIC  
15 BONE DISEASES  
17 <130> FILE REFERENCE: 1770-214PCT FC/  
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/806,110  
C--> 19 <141> CURRENT FILING DATE: 2001-03-28  
19 <150> PRIOR APPLICATION NUMBER: CA 2,245,903  
20 <151> PRIOR FILING DATE: 1998-09-28  
22 <160> NUMBER OF SEQ ID NOS: 11  
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 3130  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Unknown  
31 <220> FEATURE:  
32 <221> NAME/KEY: CDS  
33 <222> LOCATION: (604)...(2848)  
34 <223> OTHER INFORMATION: Human PEX  
W--> 35 <400> SEQUENCE: 1  
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37 atctttgatg aagacaattc aggcaagcag aatgattctt gcaacagaat tacatgatta 120  
38 attgagatct tgaagtgggt cgggtgaatc ctggccacct aacttatcat gatttggggg 180  
39 agttttcacga gaatccagtt ttgataaaac aattgttttt ttctcccca agtgactata 240  
40 catttaata gctaaaacat ctgttcagca acatagtaaa acatatatac tcggaacgct 300  
41 tgagagaaga gcctgccaac cagggacttt gctgagggag agcaccaaga taaagcaaca 360  
42 ctgtttgttt tgtctagtca ggggggaaag ccaaggcaac caatatattg gttttataa 420  
43 ttttcatttg tgaagaatta tttgagaaag ggttgcgag gggagatttc ctgacggcag 480  
44 tttcttaagc tgtccattag tagaagagca agagagcctt ggatgtcaac gcctcgctct 540  
45 tgagaccagc caccaaacca cgaaaagtga ctttcttctc gtgtgctctc tacggcctt 600  
46 ctg`atg gaa gca gaa aca ggg agc agc gtg gag act gga aag aag gcc 648  
47 Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala 15  
48 1 5 10 15  
50 aac aga ggc act cga att gcc ctg gtc gtg ttt gtc ggt ggc acc cta 696  
51 Asn Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu 30  
52 20 25 30  
54 gtt ctg ggc acg atc ctc ttt cta gtg agt caa ggt ctc tta agt ctc 744  
55 Val Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu 45  
56 35 40 45  
58 caa gct aaa cag gag tac tgc ctg aag cca gaa tgc atc gaa gcg gct 792  
59 Gln Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala 60  
60 50 55 60  
62 gct gcc atc tta agt aaa gta aat ctg tot gtg gat cct tgt gat aat 840  
63 Ala Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn

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64	65	70	75	888
66	ttc ttc cgg ttc gct tgt gat ggc tgg ata agc aat aat cca att ccc			
67	Phe Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro			95
68	80	85	90	936
70	gaa gat atg cca agc tat ggg gtt tat cct tgg ctg aga cat aat gtt			
71	Glu Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val			110
72	100	105		984
74	gac ctc aag ttg aag gaa ctt ttg gag aaa tca atc agt aga agg cgg			
75	Asp Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg			125
76	115	120		1032
78	gac acc gaa gcc ata cag aaa gcc aaa atc ctt tat tca tcc tgc atg			
79	Asp Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met			140
80	130	135		1080
82	aat gag aaa gcg att gaa aaa gca gat ggc aag cca ctg cta cac atc			
83	Asn Glu Lys Ala Ile Glu Lys Ala Asp Gly Lys Pro Leu Leu His Ile			155
84	145	150		1128
86	cta cgg cat tca cct ttc cgc tgg ccc gtg ctt gaa tct aat att ggc			
87	Leu Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly			175
88	160	165		1176
90	cct gaa ggg gtt tgg tca gag aga aag ttc agc ctt ctg cag aca ctt			
91	Pro Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu			190
92	180	185		1224
94	gca acg ttt cgt ggt caa tac agc aat tct gtg ttc atc cgt ttg tat			
95	Ala Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr			205
96	195	200		1272
98	gtg tcc cct gat gac aaa gca tcc aat gaa cat atc ttg aag ctg gac			
99	Val Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp			220
100	210	215		1320
102	caa gca aca ctc tcc ctg gcc gtg agg gaa gac tac ctt gat aac agt			
103	Gln Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser			235
104	225	230		1368
106	aca gaa gcc aag tct tat cgg gat gcc ctt tac aag ttc atg gtg gat			
107	Thr Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp			255
108	240	245		1416
110	act gcc gtg ctt tta gga gct aac agt tcc aga gca gag cat gac atg			
111	Thr Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met			270
112	260	265		1464
114	aag tca gtg ctc aga ttg gaa att aag ata gct gag ata atg att cca			
115	Lys Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro			285
116	275	280		1512
118	cat gaa aac cga acc agc gag gcc atg tac aac aaa atg aac att tct			
119	His Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser			300
120	290	295		1560
122	gaa ctg agt gct atg att ccc cag ttc gac tgg ctg ggc tac atc aag			
123	Glu Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys			315
124	305	310		1608
126	aag gtc att gac acc aga ctc tac ccc cat ctg aaa gac atc agc ccc			
127	Lys Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro			330
128	320	325		

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130	tcc gag aat gtg gtg gtc cgc gtc ccg cag tac ttt aaa gat ttg ttt	1656
131	Ser Glu Asn Val Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe	
132	340 345	
134	agg ata tta ggg tct gag aga aag aag acc att gac aac tat ttg gtg	1704
135	Arg Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Asp Asn Tyr Leu Val	
136	355 360	
138	tgg aga atg gtt tat tcc aga att cca aac ctt agc agg cgc ttt cag	1752
139	Trp Arg Met Val Tyr Ser Arg Ile Pro Asn Leu Ser Arg Arg Phe Gln	
140	370 375	
142	tat aga tgg ctg gaa ttc tca agg gta atc cag ggg acc aca act ttg	1800
143	Tyr Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu	
144	385 390	
146	ctg cct caa agg gac aaa tgt gta aac ttt att gaa agt gcc ctc cct	1848
147	Leu Pro Gln Arg Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro	
148	400 405	
150	tat gtt gtt gga aag atg ttt gta gat gtg tac ttc cag gaa gat aag	1896
151	Tyr Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys	
152	420 425	
154	aag gaa atg atg gag gaa ttg gtt gag ggc gtt cgc tgg gcc ttt att	1944
155	Lys Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile	
156	435 440	
158	gac atg cta gag aaa gaa aat gag tgg atg gat gca gga acg aaa agg	1992
159	Asp Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg	
160	450 455	
162	aaa gcc aaa gaa aag gcg aga gct gtt ttg gca aaa gtt ggc tat cca	2040
163	Lys Ala Lys Glu Lys Ala Arg Ala Val Leu Ala Lys Val Gly Tyr Pro	
164	465 470	
166	gag ttt ata atg aat gat act cat gtt aat gaa gac ctc aaa gct atc	2088
167	Glu Phe Ile Met Asn Asp Thr His Val Asn Glu Asp Leu Lys Ala Ile	
168	480 485	
170	aag ttt tca gaa gcc gac tac ttt ggc aac gtc cta caa act cgc aag	2136
171	Lys Phe Ser Glu Ala Asp Tyr Phe Gly Asn Val Leu Gln Thr Arg Lys	
172	500 505	
174	tat tta gca cag tct gat ttc ttc tgg cta aga aaa gcc gtt cca aaa	2184
175	Tyr Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys	
176	515 520	
178	aca gag tgg ttt aca aat ccg acg act gtc aat gcc ttc tac agt gca	2232
179	Thr Glu Trp Phe Thr Asn Pro Thr Val Asn Ala Phe Tyr Ser Ala	
180	530 535	
182	tcc acc aac cag atc cga ttt cca gca gga gag ctc cag aag cct ttc	2280
183	Ser Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe	
184	545 550	
186	ttt tgg gga aca gaa tat cct cga tct ctg agt tat ggt gct ata gga	2328
187	Phe Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly	
188	560 565	
190	gta att gtc gga cat gaa ttt aca cat gga ttt gat aat aat ggt aga	2376
191	Val Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg	
192	580 585	
194	aaa tat gat aaa aat gga aac ctg gat cct tgg tgg tct act gaa tca	2424

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195 Lys Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser
196          595          600          605          2472
198 gaa gaa aag ttt aag gaa aaa aca aaa tgc atg att aac cag tat agc
199 Glu Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser
200          610          615          620          2520
202 aac tat tat tgg aag aaa gct ggc tta aat gtc aag ggg aag agg acc
203 Asn Tyr Tyr Trp Lys Lys Ala Gly Leu Asn Val Lys Gly Lys Arg Thr
204          625          630          635          2568
206 ctg gga gaa aat att gct gat aat gga ggc ctg cgg gaa gct ttt agg
207 Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Arg Glu Ala Phe Arg
208          640          645          650          655          2616
210 gct tac agg aaa tgg ata aat gac aga agg cag gga ctt gag gag cct
211 Ala Tyr Arg Lys Trp Ile Asn Asp Arg Arg Gln Gly Leu Glu Glu Pro
212          660          665          670          2664
214 ctt cta cca ggc atc aca ttc acc aac aac cag ctc ttc ttc ctg agt
215 Leu Leu Pro Gly Ile Thr Phe Thr Asn Asn Gln Leu Phe Phe Leu Ser
216          675          680          685          2712
218 tat gct cat gtg agg tgc aat tcc tac aga cca gaa gct gcc cga gaa
219 Tyr Ala His Val Arg Cys Asn Ser Tyr Arg Pro Glu Ala Ala Arg Glu
220          690          695          700          2760
222 caa gtc caa att ggt gct cac agt ccc cct cag ttt agg gtc aat ggt
223 Gln Val Gln Ile Gly Ala His Ser Pro Pro Gln Phe Arg Val Asn Gly
224          705          710          715          2808
226 gca att agt aac ttt gaa gaa ttc cag aaa gct ttt aac tgt cca ccc
227 Ala Ile Ser Asn Phe Glu Glu Phe Gln Lys Ala Phe Asn Cys Pro Pro
228          720          725          730          735          2858
230 aat tcc acg atg aac aga ggc atg gac tcc tgc cga ctc t ggtagctggg
231 Asn Ser Thr Met Asn Arg Gly Met Asp Ser Cys Arg Leu
232          740          745          2918
234 acgctggttt atggcactct gagacagttg cacagtgccg gcggaggctg cactgagcct
235 tcatcgccca ttgctttagg cctggaggag ctttcatttt tagtgcattt tcattatttg
236 ggtaggtgac ctgcttgat ctagacagca tctgttcaaa gttgtagggc ttataaagtg
237 gaatataaga agaactaagt atgtttcttt agaaaatcaa accaacaata ataaatccct
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240 <210> SEQ ID NO: 2
241 <211> LENGTH: 749
242 <212> TYPE: PRT
243 <213> ORGANISM: Unknown
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Human PEX
248 <400> SEQUENCE: 2
249 Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn
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251 Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val
252          20          25          30
253 Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln
254          35          40          45
255 Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala
256          50          55          60

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257 Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe
258 65 70 75 80
259 Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu
260 85 90 95
261 Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp
262 100 105 110
263 Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp
264 115 120 125
265 Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn
266 130 135 140
267 Glu Lys Ala Ile Glu Lys Ala Asp Gly Lys Pro Leu Leu His Ile Leu
268 145 150 155 160
269 Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly Pro
270 165 170 175
271 Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu Ala
272 180 185 190
273 Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr Val
274 195 200 205
275 Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp Gln
276 210 215 220
277 Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser Thr
278 225 230 235 240
279 Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp Thr
280 245 250 255
281 Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met Lys
282 260 265 270
283 Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro His
284 275 280 285
285 Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser Glu
286 290 295 300
287 Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys Lys
288 305 310 315 320
289 Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro Ser
290 325 330 335
291 Glu Asn Val Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe Arg
292 340 345 350
293 Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Asp Asn Tyr Leu Val Trp
294 355 360 365
295 Arg Met Val Tyr Ser Arg Ile Pro Asn Leu Ser Arg Arg Phe Gln Tyr
296 370 375 380
297 Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu Leu
298 385 390 395 400
299 Pro Gln Arg Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro Tyr
300 405 410 415
301 Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys Lys
302 420 425 430
303 Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile Asp
304 435 440 445
305 Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg Lys

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## VERIFICATION SUMMARY

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Input Set : A:\1770-214PCT.TXT

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No  
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:35 M:283 W: Missing Blank Line separator, <400> field identifier